caGWAS (Cancer Genome-Wide Association Studies)

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Cancer Genome-Wide Association Studies (caGWAS) allows researchers to integrate, query, report, and analyze significant associations between genetic variations and disease, drug response or other clinical outcomes. New breakthroughs in SNP array technologies make it possible to genotype hundreds of thousands of single nucleotide polymorphisms (SNPs) simultaneously, enabling whole genome association studies. Within the Clinical Genomic Object Model (CGOM), the caIntegrator team created a domain model for Whole Genome Association Study Analysis. CGOM-caGWAS is a semantically annotated domain model that captures associations between Study, Study Participant, Disease, SNP Association Analysis, SNP Population Frequency and SNP annotations.

Following the principles of caBIG®, caGWAS APIs and web portal provide:

- A semantically annotated domain model, database schema with sample data, seasoned middleware, APIs, and web portal for GWAS data;
- platform and disease agnostic CGOM-caGWAS model and associated APIs;
- the opportunity for developers to customize the look and feel of their GWAS portal;
- a foundation of open source technologies;
- a well-tested and performance-enhanced platform, as the same software is being used to house the CGEMS data portal;
- accelerated analysis of results from various biomedical studies; and
- a single application through which researchers and bioinformaticians can access and analyze clinical and experimental data from a variety of data types, as caGWAS objects are part of the CGOM, which includes microarray, genomic, immunohistochemistry, imaging, and clinical data.

For more information visit the caGWAS wiki.